

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/868,131C
Source: IFW/b
Date Processed by STIC: 2/8/06

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 02/08/2006

PATENT APPLICATION: US/09/868,131C

TIME: 12:32:57

Input Set : A:\002.00160.ST25.txt

Output Set: N:\CRF4\02082006\I868131C.raw

3 <110> APPLICANT: Cohen, Philip
 4 Kobayashi, Takayasu
 5 Deak, Maria
 7 <120> TITLE OF INVENTION: Methods Of Activating Serum Glucocorticoid Induced Protein Kinase
 9 <130> FILE REFERENCE: 002.00160
 11 <140> CURRENT APPLICATION NUMBER: US 09/868,131C
 12 <141> CURRENT FILING DATE: 2002-04-11
 14 <150> PRIOR APPLICATION NUMBER: PCT/GB99/04232
 15 <151> PRIOR FILING DATE: 1999-12-14
 17 <150> PRIOR APPLICATION NUMBER: GB 9919676.8
 18 <151> PRIOR FILING DATE: 1999-08-19
 20 <150> PRIOR APPLICATION NUMBER: US 60/112,217
 21 <151> PRIOR FILING DATE: 1998-12-14
 23 <160> NUMBER OF SEQ ID NOS: 51
 25 <170> SOFTWARE: PatentIn version 3.1
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 367
 29 <212> TYPE: PRT
 30 <213> ORGANISM: Homo sapiens
 32 <400> SEQUENCE: 1
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 38 Asn Gly Asn Ile Asn Leu Gly Pro Ser Ala Asn Pro Asn Ala Gln Pro
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 42 Thr Asp Phe Asp Phe Leu Lys Val Ile Gly Lys Gly Asn Tyr Gly Lys
 43 35 40 45
 46 Val Leu Leu Ala Lys Arg Lys Ser Asp Gly Ala Phe Tyr Ala Val Lys
 47 50 55 60
 50 Val Leu Gln Lys Lys Ser Ile Leu Lys Lys Lys Glu Gln Ser His Ile
 51 65 70 75 80
 54 Met Ala Glu Arg Ser Val Leu Leu Lys Asn Val Arg His Pro Phe Leu
 55 85 90 95
 58 Val Gly Leu Arg Tyr Ser Phe Gln Thr Pro Glu Lys Leu Tyr Phe Val
 59 100 105 110
 62 Leu Asp Tyr Val Asn Gly Gly Glu Leu Phe Phe His Leu Gln Arg Glu
 63 115 120 125
 66 Arg Arg Phe Leu Glu Pro Arg Ala Arg Phe Tyr Ala Ala Glu Val Ala
 67 130 135 140
 70 Ser Ala Ile Gly Tyr Leu His Ser Leu Asn Ile Ile Tyr Arg Asp Leu
 71 145 150 155 160
 74 Lys Pro Glu Asn Ile Leu Leu Asp Cys Gln Gly His Val Val Leu Thr
 75 165 170 175
 78 Asp Phe Gly Leu Cys Lys Glu Gly Val Glu Pro Glu Asp Thr Thr Ser

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79          180          185          190
82 Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Arg Lys
83          195          200          205
86 Glu Pro Tyr Asp Arg Ala Val Asp Trp Trp Cys Leu Gly Ala Val Leu
87          210          215          220
90 Tyr Glu Met Leu His Gly Leu Pro Pro Phe Tyr Ser Gln Asp Val Ser
91 225          230          235          240
94 Gln Met Tyr Glu Asn Ile Leu His Gln Pro Leu Gln Ile Pro Gly Gly
95          245          250          255
98 Arg Thr Val Ala Ala Cys Asp Leu Leu Gln Ser Leu Leu His Lys Asp
99          260          265          270
102 Gln Arg Gln Arg Leu Gly Ser Lys Ala Asp Phe Leu Glu Ile Lys Asn
103          275          280          285
106 His Val Phe Phe Ser Pro Ile Asn Trp Asp Asp Leu Tyr His Lys Arg
107          290          295          300
110 Leu Thr Pro Pro Phe Asn Pro Asn Val Thr Gly Pro Ala Asp Leu Lys
111 305          310          315          320
114 His Phe Asp Pro Glu Phe Thr Gln Glu Ala Val Ser Lys Ser Ile Gly
115          325          330          335
118 Cys Thr Pro Asp Thr Val Ala Ser Ser Ser Gly Ala Ser Ser Ala Phe
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127 <211> LENGTH: 16
128 <212> TYPE: PRT
129 <213> ORGANISM: Artificial Sequence
131 <220> FEATURE:
132 <223> OTHER INFORMATION: synthetic construct
134 <400> SEQUENCE: 2
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141 <211> LENGTH: 367
142 <212> TYPE: PRT
143 <213> ORGANISM: Mus musculus
145 <400> SEQUENCE: 3
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152          20          25          30
155 Thr Asp Phe Asp Phe Leu Lys Val Ile Gly Lys Gly Asn Tyr Gly Lys
156          35          40          45
159 Val Leu Leu Ala Lys Arg Lys Ser Asp Gly Ala Phe Tyr Ala Val Lys
160          50          55          60
163 Val Leu Gln Lys Lys Ser Ile Leu Lys Asn Lys Glu Gln Asn His Ile
164 65          70          75          80
167 Met Ala Glu Arg Asn Val Leu Leu Lys Asn Val Arg His Pro Phe Leu
168          85          90          95

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171 Val Gly Leu Arg Tyr Ser Phe Gln Thr Pro Glu Lys Leu Tyr Phe Val
172          100          105          110
175 Leu Asp Tyr Val Asn Gly Gly Glu Leu Phe Phe His Leu Gln Arg Glu
176          115          120          125
179 Arg Arg Phe Leu Glu Pro Arg Ala Arg Phe Tyr Thr Ala Glu Val Ala
180          130          135          140
183 Ser Ala Ile Gly Tyr Leu His Ser Leu Asn Ile Ile Tyr Arg Asp Leu
184 145          150          155          160
187 Lys Pro Glu Asn Ile Leu Leu Asp Cys Gln Gly His Val Val Leu Thr
188          165          170          175
191 Asp Phe Gly Leu Cys Lys Glu Cys Val Glu Pro Glu Glu Thr Thr Ser
192          180          185          190
195 Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Arg Lys
196          195          200          205
199 Glu Pro Tyr Asp Arg Ala Val Asp Trp Trp Cys Leu Gly Ala Val Leu
200          210          215          220
203 Tyr Glu Met Leu His Gly Leu Pro Pro Phe Phe Asn Thr Asp Val Ala
204 225          230          235          240
207 Gln Met Tyr Glu Asn Ile Leu His Gln Pro Leu Gln Ile Pro Gly Gly
208          245          250          255
211 Arg Thr Val Ala Ala Cys Asp Leu Leu Gln Gly Leu Leu His Lys Asp
212          260          265          270
215 Gln Arg Gln Arg Leu Gly Ser Lys Glu Asp Phe Leu Asp Ile Lys Asn
216          275          280          285
219 His Met Phe Phe Ser Pro Ile Asn Trp Asp Asp Leu Tyr His Lys Arg
220          290          295          300
223 Leu Thr Pro Pro Phe Asn Pro Asn Val Glu Gly Pro Ala Asp Leu Lys
224 305          310          315          320
227 His Phe Asp Pro Glu Phe Thr Gln Glu Ala Val Ser Lys Ser Ile Gly
228          325          330          335
231 Cys Thr Pro Asp Thr Val Ala Ser Ser Ser Gly Ala Ser Ser Ala Phe
232          340          345          350
235 Leu Gly Phe Ser Tyr Ala Gln Asp Asp Asp Asp Ile Leu Asp Ser
236          355          360          365
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240 <211> LENGTH: 429
241 <212> TYPE: PRT
242 <213> ORGANISM: Homo sapiens
244 <400> SEQUENCE: 4
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250 Pro Asp Phe Ile Lys Gln Arg Arg Ala Gly Leu Asn Glu Phe Ile Gln
251          20          25          30
254 Asn Leu Val Arg Tyr Pro Glu Leu Tyr Asn His Pro Asp Val Arg Ala
255          35          40          45
258 Phe Leu Gln Met Asp Ser Pro Lys His Gln Ser Asp Pro Ser Glu Asp
259          50          55          60
262 Glu Asp Glu Arg Ser Ser Gln Lys Leu His Ser Thr Ser Gln Asn Ile
263 65          70          75          80

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266 Asn Leu Gly Pro Ser Gly Asn Pro His Ala Lys Pro Thr Asp Phe Asp
267      85      90      95
270 Phe Leu Lys Val Ile Gly Lys Gly Ser Phe Gly Lys Val Leu Leu Ala
271      100      105      110
274 Lys Arg Lys Leu Asp Gly Lys Phe Tyr Ala Val Lys Val Leu Gln Lys
275      115      120      125
278 Lys Ile Val Leu Asn Arg Lys Glu Gln Lys His Ile Met Ala Glu Arg
279      130      135      140
282 Asn Val Leu Leu Lys Asn Val Lys His Pro Phe Leu Val Gly Leu His
283 145      150      155      160
286 Tyr Ser Phe Gln Thr Thr Glu Lys Leu Tyr Phe Val Leu Asp Phe Val
287      165      170      175
290 Asn Gly Gly Glu Leu Phe Phe His Leu Gln Arg Glu Arg Ser Phe Pro
291      180      185      190
294 Glu His Arg Ala Arg Phe Tyr Ala Ala Glu Ile Ala Ser Ala Leu Gly
295      195      200      205
298 Tyr Leu His Ser Ile Lys Ile Val Tyr Arg Asp Leu Lys Pro Glu Asn
299      210      215      220
302 Ile Leu Leu Asp Ser Val Gly His Val Val Leu Thr Asp Phe Gly Leu
303 225      230      235      240
306 Cys Lys Glu Gly Ile Ala Ile Ser Asp Thr Thr Thr Thr Phe Cys Gly
307      245      250      255
310 Thr Pro Glu Tyr Leu Ala Pro Glu Val Ile Arg Lys Gln Pro Tyr Asp
311      260      265      270
314 Asn Thr Val Asp Trp Trp Cys Leu Gly Ala Val Leu Tyr Glu Met Leu
315      275      280      285
318 Tyr Gly Leu Pro Pro Phe Tyr Cys Arg Asp Val Ala Glu Met Tyr Asp
319      290      295      300
322 Asn Ile Leu His Lys Pro Leu Ser Leu Arg Pro Gly Val Ser Leu Thr
323 305      310      315      320
326 Ala Trp Ser Ile Leu Glu Glu Leu Leu Glu Lys Asp Arg Gln Asn Arg
327      325      330      335
330 Leu Gly Ala Lys Glu Asp Phe Leu Glu Ile Gln Asn His Pro Phe Phe
331      340      345      350
334 Glu Ser Leu Ser Trp Ala Asp Leu Val Gln Lys Lys Ile Pro Pro Pro
335      355      360      365
338 Phe Asn Pro Asn Val Ala Gly Pro Asp Asp Ile Arg Asn Phe Asp Thr
339      370      375      380
342 Ala Phe Thr Glu Glu Thr Val Pro Tyr Ser Val Cys Val Ser Ser Asp
343 385      390      395      400
346 Tyr Ser Ile Val Asn Ala Ser Val Leu Glu Ala Asp Asp Ala Phe Val
347      405      410      415
350 Gly Phe Ser Tyr Ala Pro Pro Ser Glu Asp Leu Phe Leu
351      420      425
354 <210> SEQ ID NO: 5
355 <211> LENGTH: 2146
356 <212> TYPE: DNA
357 <213> ORGANISM: Homo sapiens
359 <400> SEQUENCE: 5

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360 atgggttcag actttatgcc ctgaaaagat ccttccagcc ctggccatct tggacttctg      60
362 gagctaccct ggctcacagg ggtcttggtg ccttgggtgt ccccagttct tgaaaaagaat      120
364 cagcctggga ggggccacac cctgaccatc cccctttatc ccttctgaga tgtttgttag      180
366 gaagtctggg tccaggggat atcattttctt gttccatcca tgcaggggtt gcttacctcg      240
368 ggtaggaaac cctcaggcgg tggcaggtgc acaggtaggg gaggatggag agggcagtg      300
370 tgcctgaagc cctggatggg cggagctgac cccccaacac caactctatc atgcctgctc      360
372 ctccctgtcc cccagagct gcctgatcat tgctacagaa tgaactctag cccagctggg      420
374 accccaagtc cacagccctc cagggccaat gggaacatca acctggggcc ttcagccaac      480
376 ccaaagtcgg agcccacgga cttcgacttc ctcaaagtca tgggcaaagg gaactacggg      540
378 aaggtcctac tggccaagcg caagtctgat ggggcgttct atgcagtga ggtactacag      600
380 aaaaagtcca tcttaaagaa gaaagagcag agccacatca tggcagagcg cagtgtgctt      660
382 ctgaagaacg tgcggcacc cttcctcgct ggctgctgct actccttcca gacacctgag      720
384 aagctctact tcgtgctcga ctatgtcaac gggggagagc tcttcttcca cctgcagcgg      780
386 gagcgccggg tccctggagcc cggggccagg ttctacgctg ctgaggtggc cagcgccatt      840
388 ggctacctgc actccctcaa catcatttac agggatctga aaccagagaa catttctctg      900
390 gactgccagg gacacgtggt gctgacggat tttggcctct gcaaggaagg tgtagagcct      960
392 gaagacacca catccacatt ctgtggtacc cctgagtact tggcacctga agtgcttcgg      1020
394 aaagagcctt atgatcgagc agtggactgg tgggtgcttg gggcagtcct ctacgagatg      1080
396 ctccatggcc tgcgcgcctt ctacagccaa gatgtatccc agatgtatga gaacattctg      1140
398 caccagccgc tacagatccc cggaggcccg acagtggccg cctgtgacct cctgcaaagc      1200
400 cttctccaca aggaccagag gcagcggctg ggctccaaag cagactttct tgagattaag      1260
402 aaccatgtat tcttcagccc cataaactgg gatgacctgt accacaagag gctaactcca      1320
404 cccttcaacc caaatgtgac aggacctgct gacttgaagc attttgacct agagttcacc      1380
406 caggaagctg tgtccaagtc cattggctgt acccctgaca ctgtggccag cagctctggg      1440
408 gcctcaagtg cattcctggg attttcttat gcgccagagg atgatgacat cttggattgc      1500
410 tagaagagaa ggacctgtga aactactgag gccagctggg attagtaagg aattaccttc      1560
412 agctgctagg aagagcgact caaactaaca atggcttcaa cgagaagcag gtttattttt      1620
414 tccagcacat aaaagaaaaa taatgtttcg gagtccagga ctggcaggac aggtcatcag      1680
416 atactcagag gctgtatctc tgccctgcca accttgacaa atggcttcca atgttaggtt      1740
418 tgctacaaga tggttactgg agctctagct gcctattttg tgtttaggga agggaaaaatg      1800
420 gaggaaaggg gagaagagca aagggcgctt ttaaagagct ttcccaaaag ctccccccaa      1860
422 tgacttttgc ttccatctca ctaaccaccc acccctacct ggaatggagg ctgggaaatg      1920
424 tggcttattt gctgggtacg tgactatccc taataacaaa ggggttttga ccctaagaca      1980
426 ttaggggaga atgttgggta ggcagccagc cctcttttac catagggcct cctggtgttt      2040
428 ggattttgat ctcaatgtgt aaaatgacag agatgtaaca agctcatagg gtatcaatat      2100
430 ctcttattgt tctatgttga aaaaaaaaaa aaaaaaaaaa aaaaaa      2146
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434 <211> LENGTH: 2404
435 <212> TYPE: DNA
436 <213> ORGANISM: Homo sapiens
438 <400> SEQUENCE: 6
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443 tataaagttc tggtttcagt ggggaagaagt gaatggtttg tcttcaggag atatgcagag      180
445 tttgataaac tttataacac tttaaaaaaa cagtttcctg ctatggccct gaagattcct      240
447 gccaagagaa tatttgggtga taattttgat ccagatttta ttaaacaaag acgagcagga      300
449 ctaaacgaat tcattcagaa cctagttagg tatccagaac tttataacca tccagatgtc      360
451 agagcattcc ttcaaagga cagtccaaaa caccagtcag atccatctga agatgaggat      420
453 gaaagaagtt ctcagaagct acactctacc tcacagaaca tcaacctggg accgtctgga      480

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 02/08/2006
PATENT APPLICATION: US/09/868,131C TIME: 12:32:58

Input Set : A:\002.00160.ST25.txt
Output Set: N:\CRF4\02082006\I868131C.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:45; Xaa Pos. 2,3,4,5,6
Seq#:46; Xaa Pos. 2,4,5,6
Seq#:47; Xaa Pos. 2,4,5,6,7
Seq#:48; Xaa Pos. 1,7,8,10
Seq#:49; Xaa Pos. 1,2,3,4,5,6,7

VERIFICATION SUMMARY

DATE: 02/08/2006

PATENT APPLICATION: US/09/868,131C

TIME: 12:32:58

Input Set : A:\002.00160.ST25.txt

Output Set: N:\CRF4\02082006\I868131C.raw

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L:1237 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46 after pos.:0
L:1275 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47 after pos.:0
L:1314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48 after pos.:0
L:1364 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49 after pos.:0